Genetic Factors and the Directionality of Comorbid Disorders

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Getting to the root(s)

"The active ingredient in Roundup moves through the weed to kill the root."



Phenotyping SUD

Arbitrary phenotypes—ICD-m, DSM-n

Dx of substance dependence: ≥3 out of nine symptoms

→ 466 combinations

 $\sum \frac{n!}{k_i!(n-k_i)!}$

Staging—opportunistic

Mixed effects: stimulants & And a depressants

And a little bit of this'd get you up

And a little bit of that'd get you down

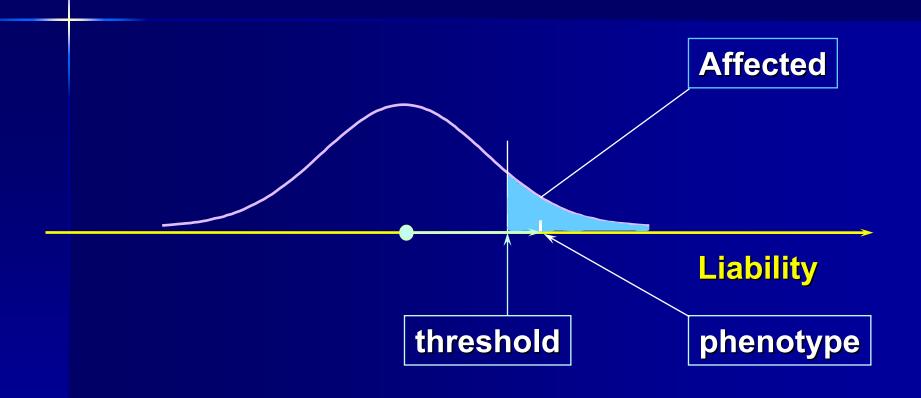
Mark Knopfler "Junkie Doll"

Liability, the concept

"...to express not only the individual innate tendency to develop or contract the disease, i.e., his susceptibility in the usual sense, but also the whole combination of external circumstances that make him more or less likely to develop the disease..."

Falconer (1965)

Liability distribution



Shared liability variance

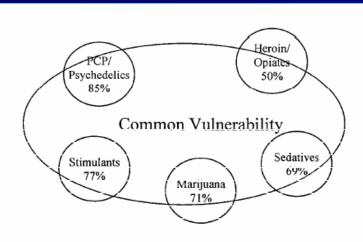


FIGURE 1. Relationship of "common vulnerability" to vulnerability for each illicit drug category.

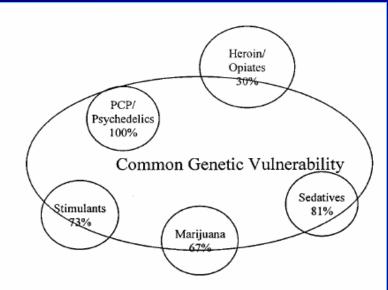
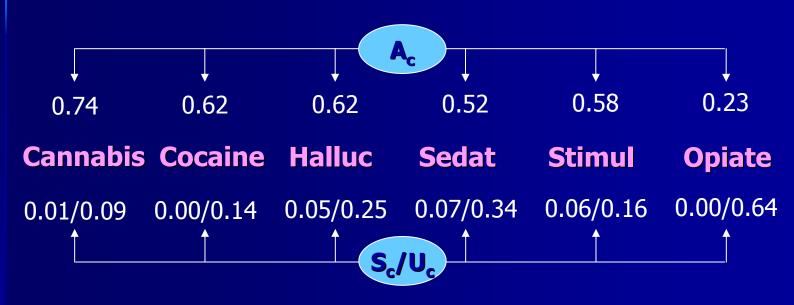


FIGURE 2. Relationship of genetic aspects of "common vulnerability" to genetic aspects of vulnerability for each illicit drug category. Proportion of variance in drug abuse attributable to genetic factors: marijuana, 33%; stimulants, 33%; sedatives, 27%; heroin/opiates, 54%; PCP/psychedelics, 26%.

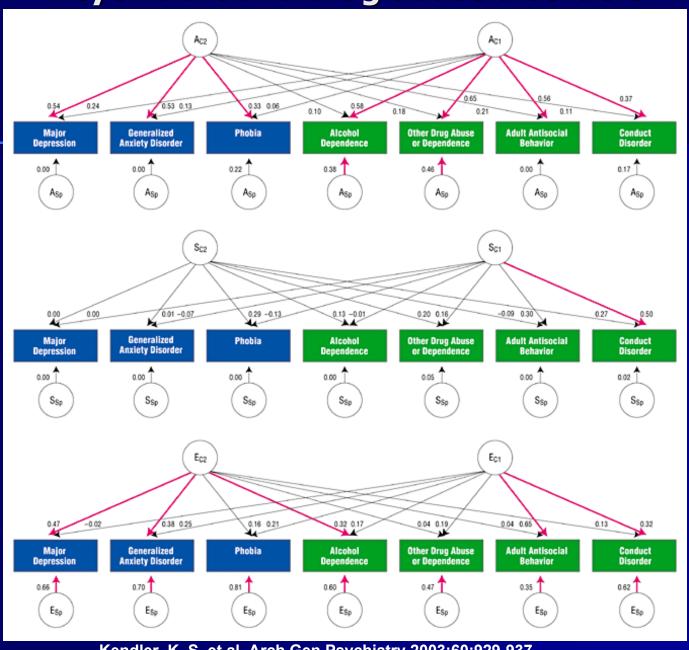
Tsuang et al., Harvard Rev Psychiatry, 9: 267-279, 2001

More sharing



Kendler et al., Am J Psychiatry 160: 687–695, 2003

Psychiatric and drug abuse disorders



Kendler, K. S. et al. Arch Gen Psychiatry 2003;60:929-937.

Common sources of variation

Pre-use

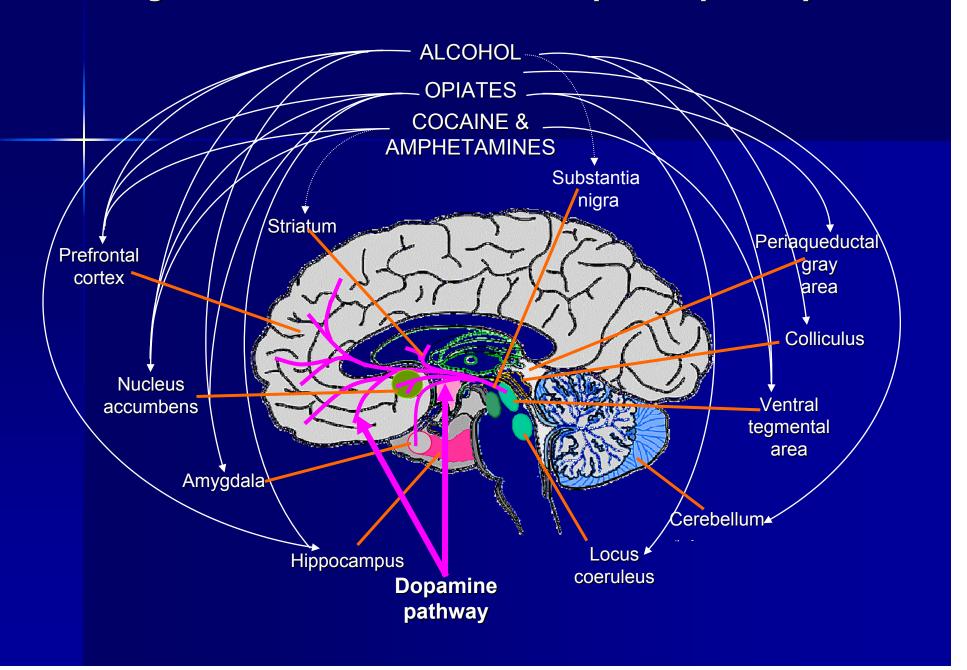
- Temperament
- Personality
- Cognition
- Behavior
- Self-medication

Post-use

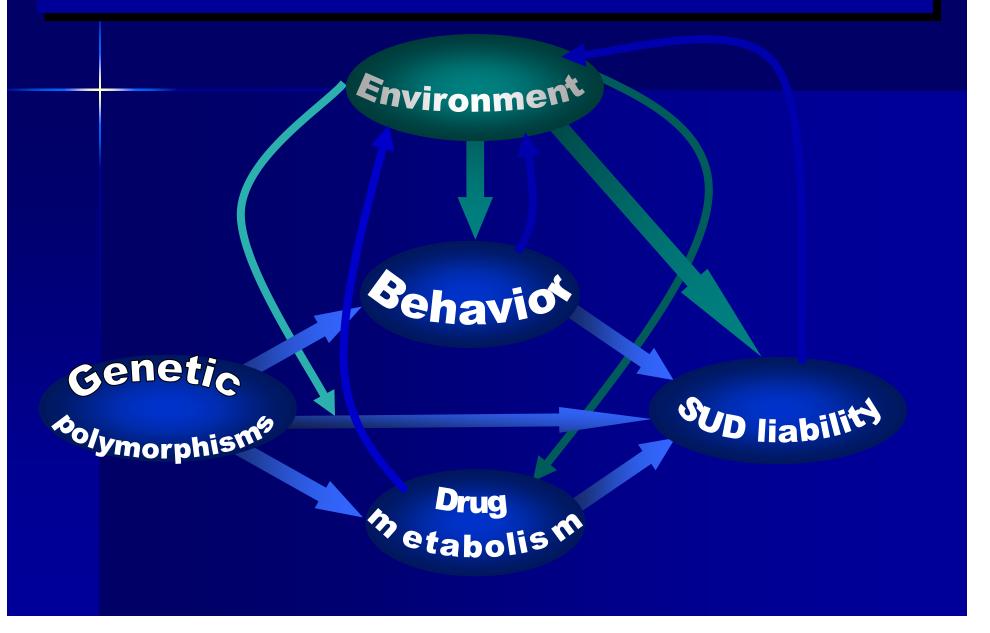
- Positive reinforcement
- Negative reinforcement

Biobehavioral self-regulation

The drug-activated mesocorticolimbic dopamine pathway



Sources of SUD risk variation

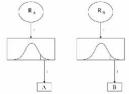


Comorbidity models

- Chance, bias, stratification
- Alternate forms (single liability)
- Multiformity (having one increases probability of another, threshold-dependent)
- Three independent
- Correlated liabilities (threshold-independent)
 - correlated
 - one causes another
 - reciprocal causation

Subsample of models

Chance



Possible Pathways for the Diagnosis of A only, B only, and AB

A only	above threshold on RA and below threshold on RB
B only	below threshold on R _A and above threshold on R _B
AB	above threshold on R, and Rn

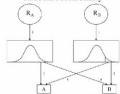
Alternate Form



Possible Pathways for the Diagnosis of A only, B only, and AB

A only	above threshold on R
B only	above threshold on R
AB	above threshold on R

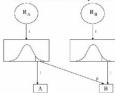
Random Multiformity



Possible Pathways for the Diagnosis of A only, B only, and AB

A only	above threshold on R _A and below threshold on R _B
B only	below threshold on RA and above threshold on RB
AB	1. above threshold on R _A and R _B 2. above threshold on R _A and below threshold on R _B

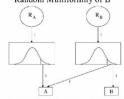
Random Multiformity of A



Bossible Bethways for the Discussio of A only B only and AB

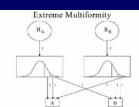
A only	above threshold on RA and below threshold on RB
B only	below threshold on RA and above threshold on RB
ΛВ	above threshold on R _A and R _B above threshold on R _A and below threshold on R _D

Random Multiformity of B



Possible Pathways for the Diagnosis of A only, B only, and AB

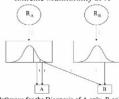
A only	above threshold on R _A and below threshold on R _B		
B only	below threshold on R_A and above threshold on R_B		
AB	1. above threshold on R _A and R _B 2. below threshold on R _A and above threshold on R _B		



Possible Pathways for the Diagnosis of A only, B only, and AB

A only	above threshold on RA and below threshold on RB
B only	below threshold on R _A and above threshold on R _B
AB	1. above threshold on R _A and R _B 2. above threshold on R _A and below threshold on R _B 3. below threshold on R _A and above threshold on R _B

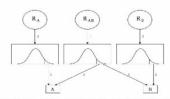
Extreme Multiformity of A



Possible Pathways for the Diagnosis of A only, B only, and AB

A only	above threshold on RA and below threshold on Ra		
B only	below threshold on RA and above threshold on RB		
AB	above threshold on R _A and R _B above threshold on R _A and below threshold on R _B		

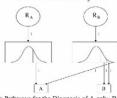
Three Independent Disorders



Possible Pathways for the Diagnosis of A only, B only, and AE

A only	above threshold on R_A and below threshold on R_B/R_{AB}		
B only	below threshold on R _A /R _{AB} and above threshold on R _B		
AB	1, above threshold on R _A and R _B		

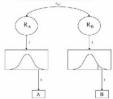
Extreme Multiformity of B



Possible Pathways for the Diagnosis of A only, B only, and Al

A only	above threshold on RA and below threshold on RB
B only	below threshold on RA and above threshold on RB
AB	1. above threshold on R _A and R _B

Correlated Liabilities



Possible Pathways for the Diagnosis of A only, B only, and AB

1	A only	above threshold on RA and below threshold on RB
	B only	below threshold on R_A and above threshold on R_B
	AB	above threshold on RA and RB

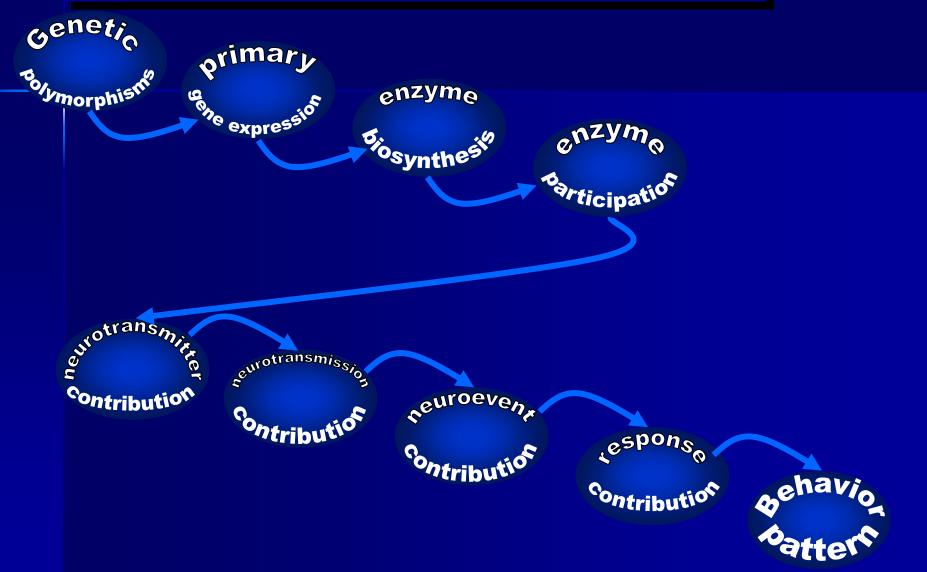
Genetics in SUD risk

Genes

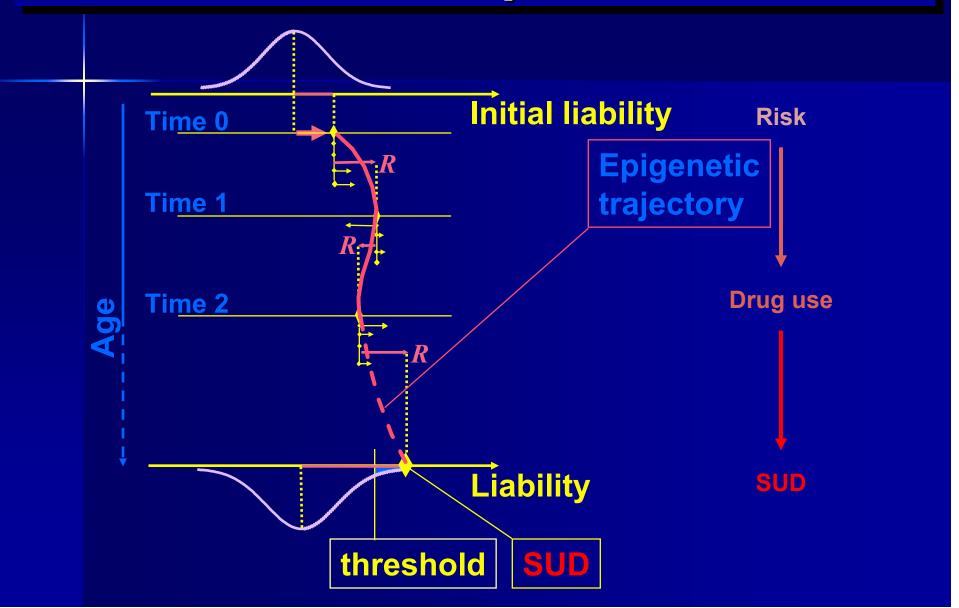
in determination in variation

SUD liability

It's a long way ...



Dynamic liability: Tracking etiology and comorbidity of SUD



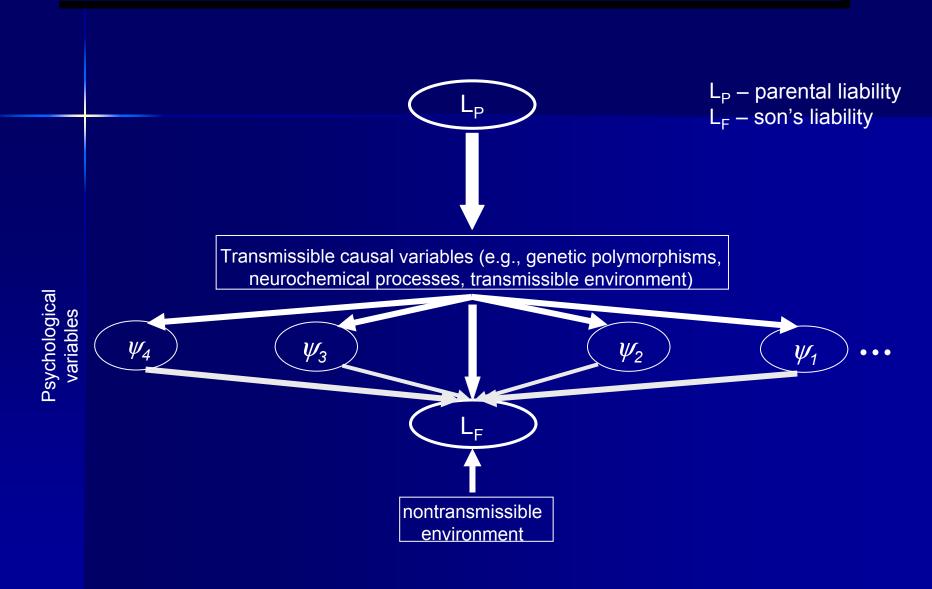
Genetics & comorbidity

- Behavior genetics
 - genetic and environmental correlations
 - developmental tracking
- Molecular genetics
 - association/linkage
 - mediation by intermediate traits
- "Hybrids"

Family history

- Faster physiological maturation
- Detachment from parents
- Homophilic peer selection/contagion
- Dysregulation/disinhibition
- Maladjustment
- SU/SUD

Determination of SUD liability

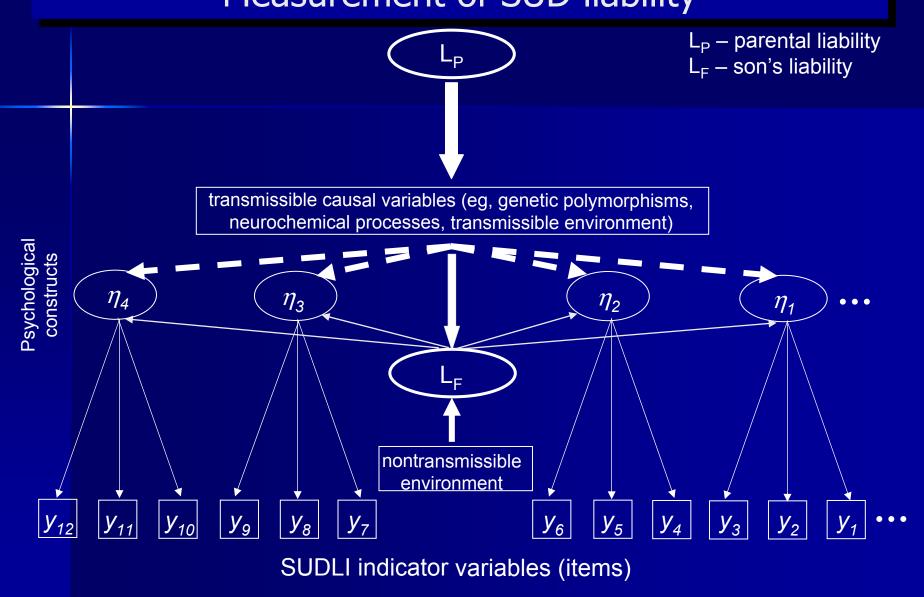


DBD and the rate of SUD

<u>Diagnosis</u>	HR	95% CI	<u>P</u>
ADHD	2.81	1.42-5.55	0.003
CD	7.17	2.78-18.52	0.00005
ODD	2.20	1.04-4.63	0.038

dysregulation

Measurement of SUD liability



DRD4-ERP-Disinhibition

- Family-based analysis (FBAT)
- Promoter region (-521) SNP
- ERP—ND: p=.02
- SNP—>P300: p=.004
- SNP—>ND: p=.003
- SNP—>ND|P300: p=.85

Parenting & MAOA

Dependent	Sample	Predictor	Hazard ratio (95% CI)	P
CD	full	dad	0.504 (0.289-0.879)	.016
		mom×dad	0.652 (0.456-0.932)	.019
	4R	dad	0.380 (0.179-0.805)	.011
		mom	1.601 (0.989-2.591)	.055
	3R	dad	0.796 (0.343-1.850)	.597
		mom	1.099 (0.534-2.265)	.797
ADHD	full	mom×dad	1.558 (1.031-2.353)	.035
		dad×MAO	3.299 (1.479-7.356)	.004
	4R	dad	1.974 (1.230-3.168)	.005
		mom×dad	1.799 (1.057-3.062)	.030
	3R	dad	0.574 (0.256-1.284)	.177
		mom×dad	1.604 (0.719-3.578)	.249
SUD	full	MAO	0.382 (0.155-0.940)	.036

Vanyukov et al. (in press) Psychiatric Genetics

MAOA & SUD

Low activity

- increase in the risk
- limbic volume reductions, hyperresponsive amygdala during emotional arousal, diminished reactivity of regulatory prefrontal regions (Meyer-Lindenberg et al., 2006)

Drug use severity

Trait Drug Use Screening Inventory

substance use problems scale

Sample 94 male Caucasian adolescents

(12-18 years of age) with a

DSM-IV diagnosis of Substance

Dependence related to illicit

drugs

Genes Polymorphisms in DRD1-DRD5

genes

Analysis Two-way ANOVA, testing main

effects and interactions

between D1- and D2-family

genes

Interactions as expected

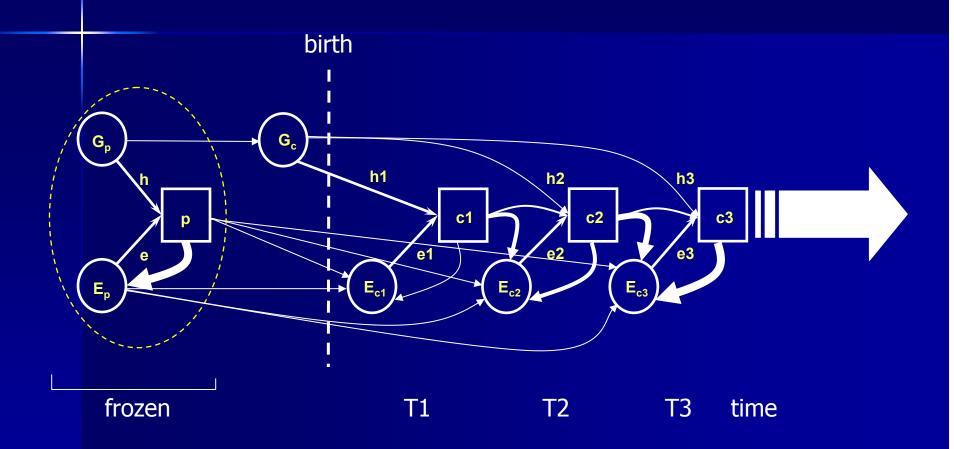
Predictor sets	df	F	p
DRD1.1	2	2.28	.108
DRD2	1	0.02	.898
DRD1.1×DRD2	1	4.39	.039
DRD1.1	2	3.63	.031
DRD3	4	1.09	.369
DRD1.1×DRD3	6	2.29	.044
DRD1.7	2	4.47	.015
DRD3	4	0.72	.584
DRD1.7×DRD3	6	2.60	.025

Candidate system genes

Comorbidity helps: multiple hits

- cross-verify
- identify pathways
- support the gene's role

Dynamic



Note: G×E omitted

Genetic roots

... environmental "Roundup"?

